

BLAST**Basic Local Alignment Search Tool**

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Nucleotide Sequence (4347 letters)

SEQ ID NO: 1

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|31285

lcl|31285

Description

None

Molecule type

nucleic acid

Query Length

4347

Database Name

nr

Description

All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

ProgramBLASTN 2.2.22+ [Citation](#)**Reference**

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#)

[Search Parameters](#)

Search parameter name Search parameter value

Program	blastn
Word size	28
Expect value	10
Hitlist size	100
Match/Mismatch scores	1,-2
Gapcosts	0,0
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Database

Database parameter name Database parameter value

Posted date	Feb 18, 2010 5:42 PM
Number of letters	30,229,719,529
Number of sequences	10,937,181
Entrez query	none

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	1.33271	1.28
K	0.620991	0.46
H	1.12409	0.85

Results Statistics

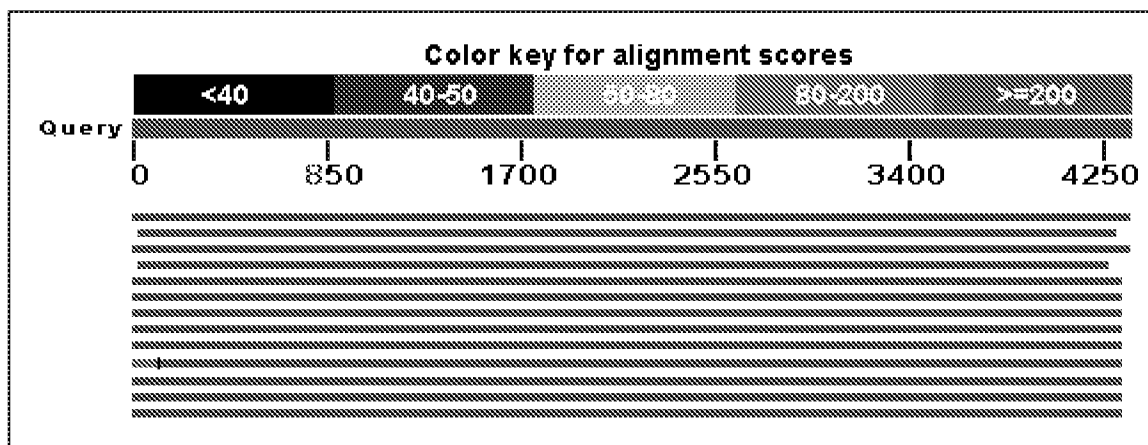
Results Statistics parameter name Results Statistics parameter value

Length adjustment	35
Effective length of query	4312
Effective length of database	29846918194
Effective search space	128699911252528
Effective search space used	128699911252528

[Graphic Summary](#)**Distribution of 107 Blast Hits on the Query Sequence**

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.












Descriptions

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

AF063497.1	Adeno-associated virus 1, complete genome	6575	6575	99%	0.0	94%	
DQ180604.1	Adeno-associated virus VR-195 Rep78 (rep78) and capsid protein (cap) genes, complete cds	6312	6312	97%	0.0	93%	
AF028704.1	Adeno-associated virus 6, complete genome	6270	6270	99%	0.0	92%	
DQ180605.1	Adeno-associated virus VR-355 Rep78 (rep78) and capsid protein (cap) genes, complete cds	6139	6139	97%	0.0	92%	
AF043303.1	Adeno-associated virus 2, complete genome	5142	5142	99%	0.0	88%	
J01901.1	Adeno-associated virus 2, complete genome	5105	5105	99%	0.0	88%	
AY695374.1	Adeno-associated virus isolate hu.T71 Rep78 protein and capsid protein VP1 (cap) genes, complete cds	5005	5005	99%	0.0	87%	
AY695372.1	Adeno-associated virus isolate hu.T40 Rep78 protein and capsid protein VP1 (cap) genes, complete cds	5003	5003	99%	0.0	87%	
AY695371.1	Adeno-associated virus isolate hu.T32 Rep78 protein and capsid protein VP1 (cap) genes, complete cds	4937	4937	99%	0.0	87%	
AF369963.1	Cloning vector pAAV-RC, complete sequence	4922	5100	99%	0.0	93%	
AY695376.1	Adeno-associated virus isolate hu.S17 Rep78 protein and capsid protein VP1 (cap) genes, complete cds	4911	4911	99%	0.0	87%	
AY695375.1	Adeno-associated virus isolate hu.T88 Rep78 protein and capsid protein VP1 (cap) genes, complete cds	4859	4859	99%	0.0	87%	
AY695373.1	Adeno-associated virus isolate hu.T70 Rep78 protein and capsid protein VP1 (cap) genes, complete cds	4837	4837	99%	0.0	87%	
AF513851.1	Adeno-associated virus 7 nonstructural protein and capsid protein genes, complete cds	4595	4595	99%	0.0	86%	
AF513852.1	Adeno-associated virus 8 nonstructural protein and capsid protein genes, complete cds	4346	4346	98%	0.0	85%	
AY631965.1	Adeno-associated virus 10 nonstructural protein and capsid protein genes, complete cds	4152	4152	94%	0.0	85%	
EU368918.1	Adeno-associated virus isolate hu.48R3 capsid protein VP1 gene, partial cds	4050	4050	50%	0.0	99%	
AY530611.1	Adeno-associated virus isolate hu.48 capsid protein VP1 (cap) gene, complete cds	4039	4039	50%	0.0	99%	
EU285562.1	Adeno-associated virus 13 nonstructural protein and capsid protein genes, complete cds	3903	3903	96%	0.0	83%	
AF028705.1	Adeno-associated virus 3B, complete genome	3869	3869	98%	0.0	83%	
U48704.1	Adeno-associated virus 3 nonstructural protein and capsid protein genes, complete cds, and complete genome	3829	3829	98%	0.0	83%	
AY530606.1	Adeno-associated virus isolate hu.43 capsid protein VP1 (cap) gene, complete	3825	3825	50%	0.0	97%	


	cds							
EU368917.1	Adeno-associated virus isolate hu.44r3 capsid protein VP1 gene, partial cds	3773	3773	50%	0.0	97%		
EU368916.1	Adeno-associated virus isolate hu.44R2 capsid protein VP1 gene, partial cds	3773	3773	50%	0.0	97%		
AY530607.1	Adeno-associated virus isolate hu.44 capsid protein VP1 (cap) gene, complete cds	3768	3768	50%	0.0	97%		
AY530609.1	Adeno-associated virus isolate hu.46 capsid protein VP1 (cap) gene, complete cds	3735	3735	50%	0.0	97%		
EU368911.1	Adeno-associated virus isolate AAV6R2 capsid protein VP1 gene, partial cds	3729	3729	50%	0.0	97%		
EU368910.1	Adeno-associated virus isolate AAV6.2 capsid protein VP1 gene, partial cds	3723	3723	50%	0.0	97%		
EU368909.1	Adeno-associated virus isolate AAV6.1 capsid protein VP1 gene, partial cds	3723	3723	50%	0.0	97%		
J01902.1	adeno-associated virus 2 left half 45% of genome	3349	3349	44%	0.0	98%		
EU048698.1	Shuttle vector phcAd.DYS-FL, complete sequence	2918	3123	39%	0.0	100%		
AY631966.1	Adeno-associated virus 11 nonstructural protein and capsid protein genes, complete cds	2865	3171	70%	0.0	88%		
GQ380656.1	Expression shuttle vector pGAPDH.Rep68, complete sequence	2835	2835	36%	0.0	98%		
GQ380657.1	Expression shuttle vector pGAPDH.Rep68 (Y156F), complete sequence	2830	2830	36%	0.0	98%		
DQ813647.1	Adeno-associated virus 12 Rep78 and VP1 genes, complete cds	2446	2740	71%	0.0	85%		
U89790.1	Adeno-associated virus 4, complete genome	2442	2827	73%	0.0	84%		
AY530567.1	Adeno-associated virus isolate rh.54 capsid protein VP1 (cap) gene, complete cds	2307	2307	50%	0.0	85%		
EU368920.1	Adeno-associated virus isolate rh.37R2 capsid protein VP1 gene, partial cds	2257	2257	50%	0.0	85%		
AY243000.1	Non-human primate Adeno-associated virus isolate AAVrh.35 capsid protein (VP1) gene, complete cds	2257	2257	50%	0.0	85%		
AY242999.1	Non-human primate Adeno-associated virus isolate AAVrh.36 capsid protein (VP1) gene, complete cds	2252	2252	50%	0.0	85%		
AY242998.1	Non-human primate Adeno-associated virus isolate AAVrh.37 capsid protein (VP1) gene, complete cds	2246	2246	50%	0.0	85%		
AY242997.1	Non-human primate Adeno-associated virus isolate AAVrh.8 capsid protein (VP1) gene, complete cds	2244	2244	50%	0.0	85%		
EU368925.1	Adeno-associated virus isolate rh.8R capsid protein VP1 gene, partial cds	2242	2242	50%	0.0	85%		
AY530568.1	Adeno-associated virus isolate rh.55 capsid protein VP1 (cap) gene, complete cds	2235	2235	50%	0.0	85%		
EU368923.1	Adeno-associated virus isolate rh.48R2 capsid protein VP1 gene, partial cds	2213	2213	50%	0.0	85%		
AY243020.1	Non-human primate Adeno-associated virus isolate AAVcy.2 capsid protein (VP1)	2213	2213	50%	0.0	85%		

	gene, complete cds						
AY530561.1	Adeno-associated virus isolate rh.48 capsid protein VP1 (cap) gene, complete cds	2191	2191	50%	0.0	84%	
AY530571.1	Adeno-associated virus isolate rh.60 capsid protein VP1 (cap) gene, complete cds	2185	2185	50%	0.0	84%	
EU368922.1	Adeno-associated virus isolate rh.46 capsid protein VP1 gene, partial cds	2167	2167	50%	0.0	84%	
AY530560.1	Adeno-associated virus isolate rh.43 capsid protein VP1 (cap) gene, complete cds	2167	2167	50%	0.0	84%	
AY530573.1	Adeno-associated virus isolate rh.62 capsid protein VP1 (cap) gene, complete cds	2163	2163	50%	0.0	84%	
AY243006.1	Non-human primate Adeno-associated virus isolate AAVrh.22 capsid protein (VP1) gene, complete cds	2161	2161	50%	0.0	84%	
EU368924.1	Adeno-associated virus isolate rh.64R1 capsid protein VP1 gene, partial cds	2156	2156	50%	0.0	84%	
AY530574.1	Adeno-associated virus isolate rh.64 capsid protein VP1 (cap) gene, complete cds	2150	2150	50%	0.0	84%	
AY530562.1	Adeno-associated virus isolate rh.49 capsid protein VP1 (cap) gene, complete cds	2150	2150	50%	0.0	84%	
AY530572.1	Adeno-associated virus isolate rh.61 capsid protein VP1 (cap) gene, complete cds	2145	2145	50%	0.0	84%	
AY530566.1	Adeno-associated virus isolate rh.53 capsid protein VP1 (cap) gene, complete cds	2145	2145	50%	0.0	84%	
AY530565.1	Adeno-associated virus isolate rh.52 capsid protein VP1 (cap) gene, complete cds	2145	2145	50%	0.0	84%	
AY530563.1	Adeno-associated virus isolate rh.50 capsid protein VP1 (cap) gene, complete cds	2145	2145	50%	0.0	84%	
EU368919.1	Adeno-associated virus isolate rh.2R capsid protein VP1 gene, partial cds	2139	2139	50%	0.0	84%	
AY530601.1	Adeno-associated virus isolate hu.39 capsid protein VP1 (cap) gene, complete cds	2134	2134	50%	0.0	84%	
AY530569.1	Adeno-associated virus isolate rh.57 capsid protein VP1 (cap) gene, complete cds	2122	2122	50%	0.0	84%	
AY530564.1	Adeno-associated virus isolate rh.51 capsid protein VP1 (cap) gene, complete cds	2122	2122	50%	0.0	84%	
AY243015.1	Non-human primate Adeno-associated virus isolate AAVrh.10 capsid protein (VP1) gene, complete cds	2122	2122	50%	0.0	84%	
AY243007.1	Non-human primate Adeno-associated virus isolate AAVrh.2 capsid protein (VP1) gene, complete cds	2122	2122	50%	0.0	84%	
EU368921.1	Adeno-associated virus isolate rh.39 capsid protein VP1 gene, partial cds	2111	2111	50%	0.0	84%	
AY530559.1	Adeno-associated virus isolate rh.40 capsid protein VP1 (cap) gene, complete cds	2111	2111	50%	0.0	84%	

	cds						
AY243008.1	Non-human primate Adeno-associated virus isolate AAVrh.19 capsid protein (VP1) gene, complete cds	2108	2108	50%	0.0	84%	
AY243013.1	Non-human primate Adeno-associated virus isolate AAVrh.13 capsid protein (VP1) gene, complete cds	2106	2106	50%	0.0	84%	
EU368914.1	Adeno-associated virus isolate cy.5R4 capsid protein VP1 gene, partial cds	2100	2100	50%	0.0	84%	
AY530627.1	Adeno-associated virus isolate hu.67 capsid protein VP1 (cap) gene, complete cds	2095	2095	50%	0.0	84%	
AY530605.1	Adeno-associated virus isolate hu.42 capsid protein VP1 (cap) gene, complete cds	2095	2095	50%	0.0	84%	
AY530603.1	Adeno-associated virus isolate hu.40 capsid protein VP1 (cap) gene, complete cds	2095	2095	50%	0.0	84%	
AY530600.1	Adeno-associated virus isolate hu.37 capsid protein VP1 (cap) gene, complete cds	2095	2095	50%	0.0	84%	
AY530582.1	Adeno-associated virus isolate hu.17 capsid protein VP1 (cap) gene, complete cds	2095	2095	50%	0.0	84%	
AY530557.1	Adeno-associated virus isolate rh.25 capsid protein VP1 (cap) gene, complete cds	2095	2095	50%	0.0	84%	
AY243023.1	Non-human primate Adeno-associated virus isolate AAVbb.1 capsid protein (VP1) gene, complete cds	2095	2095	50%	0.0	84%	
AY243022.1	Non-human primate Adeno-associated virus isolate AAVbb.2 capsid protein (VP1) gene, complete cds	2095	2095	50%	0.0	84%	
EU368913.1	Adeno-associated virus isolate cy.1R1 capsid protein VP1 gene, partial cds	2084	2084	50%	0.0	84%	
AY530626.1	Adeno-associated virus isolate hu.66 capsid protein VP1 (cap) gene, complete cds	2084	2084	50%	0.0	84%	
AY530621.1	Adeno-associated virus isolate hu.6 capsid protein VP1 (cap) gene, complete cds	2084	2084	50%	0.0	84%	
AY530570.1	Adeno-associated virus isolate rh.58 capsid protein VP1 (cap) gene, complete cds	2084	2084	50%	0.0	84%	
AY243018.1	Non-human primate Adeno-associated virus isolate AAVcy.4 capsid protein (VP1) gene, complete cds	2084	2084	50%	0.0	84%	
AY243017.1	Non-human primate Adeno-associated virus isolate AAVcy.5 capsid protein (VP1) gene, complete cds	2084	2084	50%	0.0	84%	
AY243016.1	Non-human primate Adeno-associated virus isolate AAVcy.6 capsid protein (VP1) gene, complete cds	2084	2084	50%	0.0	84%	
AY530604.1	Adeno-associated virus isolate hu.41 capsid protein VP1 (cap) gene, complete cds	2078	2078	50%	0.0	84%	
AY530558.1	Adeno-associated virus isolate rh.38 capsid protein VP1 (cap) gene, complete cds	2078	2078	50%	0.0	84%	

AY243019.1	Non-human primate Adeno-associated virus isolate AAVcy.3 capsid protein (VP1) gene, complete cds	2078	2078	50%	0.0	84%
AY530556.1	Adeno-associated virus isolate rh.1 capsid protein VP1 (cap) gene, complete cds	2063	2063	50%	0.0	84%
AY243012.1	Non-human primate Adeno-associated virus isolate AAVrh.14 capsid protein (VP1) gene, complete cds	2052	2052	50%	0.0	83%
AY243004.1	Non-human primate Adeno-associated virus isolate AAVrh.24 capsid protein (VP1) gene, complete cds	2052	2052	50%	0.0	83%
AY243009.1	Non-human primate Adeno-associated virus isolate AAVrh.18 capsid protein (VP1) gene, complete cds	2023	2023	50%	0.0	83%
AY243011.1	Non-human primate Adeno-associated virus isolate AAVrh.16 capsid protein (VP1) gene, complete cds	1980	1980	50%	0.0	83%
AY243005.1	Non-human primate Adeno-associated virus isolate AAVrh.23 capsid protein (VP1) gene, complete cds	1906	1976	46%	0.0	90%
EU368912.1	Adeno-associated virus isolate ch.5R capsid protein VP1 gene, partial cds	1829	1829	50%	0.0	82%
AY243021.1	Non-human primate Adeno-associated virus isolate AAVch.5 capsid protein (VP1) gene, complete cds	1829	1829	50%	0.0	82%
AF383623.1	Cloning vector pREX1LC, complete sequence	1812	3202	44%	0.0	99%
AY530585.1	Adeno-associated virus isolate hu.2 capsid protein VP1 (cap) gene, complete cds	1777	1777	50%	0.0	81%
AY530602.1	Adeno-associated virus isolate hu.4 capsid protein VP1 (cap) gene, complete cds	1770	1770	50%	0.0	81%
AY530575.1	Adeno-associated virus isolate hu.1 capsid protein VP1 (cap) gene, complete cds	1764	1764	50%	0.0	81%

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)

>**gb|AF063497.1|AF063497**  Adeno-associated virus 1, complete genome
Length=4718

Score = 6575 bits (3560), Expect = 0.0
Identities = 4107/4368 (94%), Gaps = 49/4368 (1%)
Strand=Plus/Plus

Query	6	GTCCTGTATTAGAGGTCACGTGAGTG-TTTTGCACATTTTGCACACCAITGTGGTCACG	64
Sbjct	205CT.....C.....C....C...-T	263
Query	65	CT-GGGTATTTAAGCCCGAGTGAGC-ACGCAGGGTCTCCATTTTGAAGCGGGAGGTTTGA	122
Sbjct	264	T.A.....A..T.G.....G.-.....A.....~.C..C..AA.....	321
Query	123	ACGCGCAGCCGCCATGCCGGGGTTTTACGAGATTGTGATTAAAGGTCCCCAGCGACCTTGA	182
Sbjct	322	...A.....A.....C..C.....C.....C.....G..G.....G..	381
Query	183	CGGGCATCTGCCCCGGCATTCTGACAGC-TTTGTGAACTGGGTGGCCGAGAAGGAATGGG	241
Sbjct	382	..A...C.....G.....-T.G.....G.....	440
Query	242	AGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGACCGTGG	301
Sbjct	441	..C....C..G.....	500
Query	302	CCGAGAAGCTGCAGCGCGACTTTCT-GACGGAATGGCGCCGTGTGAGTAAGGCCCCGGAG	360
Sbjct	501C..G.T.-C.....C.....	559
Query	361	GCCCTTTTCTTTGTGCAATTIGAGAAGGGAGAGAGCTACTTCCACATGCACGTGCTCGTG	420
Sbjct	560C.....T..G..C.....C...TC.....C.C..TA.T..G...	619
Query	421	GAAACCACCGGGGTGAAATCCATGGTTTTGGGACGTTTCCTGAGTCAGATTCGCGAAAAA	480
Sbjct	620	..G.....G.....C.....GC....C..C.....A.G..C..G	679
Query	481	CTGATTGAGAGAATTTACCGCGGGATCGAGCCGACTTTGCCAAACTGGTTTCGCGGTACACA	540
Sbjct	680	...G.G....CC..C.....CC....C.....G..C	739
Query	541	AAGAC-CAGAAATGGCGCCGGAGGCGGGAACAAGGTGGTGATGAGTGCTACATCCCCAA	599
Sbjct	740G.-.T.....G.....C.....	798
Query	600	TTACTTGCTCCCCAAAACCCAGCCTGAGCTCCAGTGGGCGTGGACTAATATGGAACAGTA	659
Sbjct	799	C...C.C..G.....G..T.....C.....G.....C.....GG....	858
Query	660	TTTAAGCGCCTGTTTGAATCTCACGGAGCGTAAACGGTTGGTGGCGCAGCATCTGACGCA	719
Sbjct	859	.A.....C..GG.C.....C.....C.C.....C.....C..	918
Query	720	CGTGTC-G-CAGACGCAGGAGCAGAACAAAGAGAATCAGAATCCCAATTCTGATGCGCCG	777
Sbjct	919	.-...A.C.....C.....G.....T..C.....C.....T	976
Query	778	GTGATCAGATCAAAAACCTTCAGC-CAGGTACATGGAGCTGGTCGGGTGGCTCGTGACAA	836
Sbjct	977	..C...C.G.....C..C..G.-.C.....G.....-C	1034
Query	837	GGGG-ATTACCTCGGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCATACATCTCCTTCA	895
Sbjct	1035C..C.....C.....G.....	1094
Query	896	ATGCGGCCTCCAACCTCGCGGTCCCAAATCAAGGCTGCCT-TGGACAATGCGGGAAAGATT	954
Sbjct	1095	.C..C..T.....G.....C.-.C.....C..C.....C	1153
Query	955	ATGAGC-CTGACTAAAACCGCCCCCGACTACCTGGTGGGCCAGCAGC-CCG-TGGAGGAC	1011
Sbjct	1154	...-.G.....C...T...G.....A.....-C..T...CCC.C....	1210

Query	1012	ATTTCAGCAATCGGATTTATAAAATTTTGGAACTAAACGGGTACGATCC--CCAATATG	1069
Sbjct	1211	...AAA.C...C..C..C..CCGC..CC....G..G.....C.....A..TG..-...C.	1268
Query	1070	-CGGCTTCCGTCTTTCTGGGATGGG-CCACGAAAAAGTTCGGCAAGAGGAACACCATCTG	1127
Sbjct	1269	C....-.....C..C....C...-.....G.....G...C.C.....	1326
Query	1128	GCTGTTTGGGCCTGCAACTACCGGG-AAGACCAACATCGCGGAGGCCATAGCCACACTG	1186
Sbjct	1327G..C..C.-.....C.....A.....C.....G.C.	1385
Query	1187	TGCCCTTCTACGGGTGCGTAAACTGGACCAATGAGAACTTTCCTTCAACGACTGTGTCTG	1246
Sbjct	1386C.....C.....T..T..C....	1445
Query	1247	ACAAGATGGTGATCTGGTGGGAGGAGGGGAAGATGACCGCCAAGGTCGTGGAGTCGGCCA	1306
Sbjct	1446C.....G.....C....	1505
Query	1307	AAGCCATTCTGGGAGGAAGCAAGGTGCGCGTGGACCAGAAA-TGCAAGTCCTCGGCCAG	1365
Sbjct	1506	.G.....C..C..C.....-...G.....G..C.....	1564
Query	1366	ATAGACCCGACTCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGG	1425
Sbjct	1565	..C.....C..C.....	1624
Query	1426	AAC-TCAACGACCTTCGAACACCAGCAGCCGTTGCAAGACCGGATGTTCAAATTTGAACT	1484
Sbjct	1625	...AG.-..C.....G.....G.....	1683
Query	1485	CACCCGCCGTCTGGATCATGACTTTGGGAAGGTCACCAAGCAGGAAGTCAAAGACTTTTT	1544
Sbjct	1684G.....C.....G..A.....G..C..	1743
Query	1545	CCGGTGGGCAAAGGATCACGTGGTTGAGGTGGAGCATGAATTCTACGTCAAAAAGGGTGG	1604
Sbjct	1744	...C.....GC.....ACC.....C.....G.....G.....	1803
Query	1605	AGCCAAGAAAAGACCCGCCCCCAG-TGACGCAGATATAAGTGAGCCCAAACGGGTGC-GC	1662
Sbjct	1804C.....-..A.....G....A...C.....G....-C.T..	1861
Query	1663	GAGTCAGTTGCGCAGCCATCGACGTCAGACGCGG-A--AGCTTCGATCAACTACGCAGAC	1719
Sbjct	1862	CCC.....C...G.T.....A.GG....C..G.GG...TT..C...	1921
Query	1720	AGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAG	1779
Sbjct	1922	1981
Query	1780	ACATGCGAGAGAATGAATCAGAATTTCAACATTTGCTTCACGCACGGGACGAGAGACTGT	1839
Sbjct	1982	2041
Query	1840	TCAGAGTGCTTCCCCGGCGTGTGAGAATCTCAACCGGTCTGTCAGAAAGAGGACGTATCGG	1899
Sbjct	2042	2101
Query	1900	AAACTCTGTGCCATTTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGC	1959
Sbjct	2102	2161
Query	1960	GATCTGGTCAACGTGGACCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGG	2019
Sbjct	2162	2221
Query	2020	TATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCTG	2079
Sbjct	2222	2281
Query	2080	CGAGTGGTGGGACTTGAAACCTGGAGCCCCGAAGCCCAAAGCCAACCAGCAAAAGCAGGA	2139
Sbjct	2282	2341
Query	2140	CGACGGCCGGGTCTGGTGCTTCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGA	2199
Sbjct	2342	2401
Query	2200	CAAGGGGGAGCCCGTCAACGCGGCGGACGCAGCGGCCCTCGAGCACGACAAGGCCTACGA	2259
Sbjct	2402	2461
Query	2260	CCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTT	2319
Sbjct	2462	2521
Query	2320	TCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGCAGTCTTCCA	2379
Sbjct	2522	2581
Query	2380	GGCCAAGAAGCGGGTTCTCGAACCTCTCGGTCTGGTTGAGGAAGGCGCTAAGACGGCTCC	2439
Sbjct	2582	2641
Query	2440	TGGAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATCGG	2499
Sbjct	2642	2701
Query	2500	CAAGACAGGCCAGCAGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGA	2559
Sbjct	2702	2761
Query	2560	GTCAGTCCCCGATCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACC	2619
Sbjct	2762	2821

Query	2620	TACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGG	2679
Sbjct	2822	2881
Query	2680	AGTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCAT	2739
Sbjct	2882	2941
Query	2740	CACCACCAGCACCCGCACCTGGGCCTTGCCACCTACAATAACCACCTCTACAAGCAAAT	2799
Sbjct	2942	3001
Query	2800	CTCCAGTGCTTCAACGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTG	2859
Sbjct	3002	3061
Query	2860	GGGGTATTTTGTATTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGACT	2919
Sbjct	3062	3121
Query	2920	CATCAACAACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAAACCTTTCAACATCCA	2979
Sbjct	3122	3181
Query	2980	AGTCAAGGAGGTCACGACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCAGCAC	3039
Sbjct	3182	3241
Query	3040	GGTTCAAGTCTTCTCGGACTCGGAGTACCAGCTTCCGTACGTCCTCGGCTCTGCGCACCA	3099
Sbjct	3242	3301
Query	3100	GGGCTGCCTCCCTCCGTTCCCGGCGGACGTGTTTCATGATTCCGCAATACGGCTACCTGAC	3159
Sbjct	3302	3361
Query	3160	GCTCAACAATGGCAGCCAAGCCGTGGGACGTTTCATCCTTTTACTGCCTGGAATATTTCCC	3219
Sbjct	3362	3421
Query	3220	TTCTCAGATGCTGAGAACGGGCAACAACCTTTACCTTCAGCTACACCTTTGAGGAAGTGCC	3279
Sbjct	3422	3481
Query	3280	TTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGA	3339
Sbjct	3482	3541
Query	3340	CCAATACCTGTATTACCTGAACAGAACTCAAAATCAGTCCGGAAGTGCCAAAACAAGGA	3399
Sbjct	3542	3601
Query	3400	CTTGCTGTTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTTCAGCCCAAAACTGGCTACC	3459
Sbjct	3602	3661
Query	3460	TGGACCCTGTTATCGGCAGCAGCGCTTTCTAAAACAAAAACAGACAACAACAACAGCAA	3519
Sbjct	3662	3721
Query	3520	TTTTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGGCGTGAATCCATCATCAACCC	3579
Sbjct	3722	3781
Query	3580	TGGCACTGCTATGGCCTCACACAAAGACGACGAAGACAAGTTCTTTCCCATGAGCGGTGT	3639
Sbjct	3782	3841
Query	3640	CATGATTTTTTGAAAAGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGAT	3699
Sbjct	3842	3901
Query	3700	TACAGACGAAGAGGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGACCGT	3759
Sbjct	3902	3961
Query	3760	GGCAGTCAATTTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGCTATGGG	3819
Sbjct	3962	4021
Query	3820	AGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTGTTGGC	3879
Sbjct	4022	4081
Query	3880	CAAAATTCCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGGCGGCTTTGGACT	3939
Sbjct	4082	4141
Query	3940	CAAGAACCCGCCTCCTCAGATCCTCATAAAAACACGCCTGTTCTGCGAATCCTCCGGC	3999
Sbjct	4142	4201
Query	4000	GGAGTTTTTCAGCTACAAAGTTTGCTTCATTTCATACCCAATACTCCACAGGACAAGTGAG	4059
Sbjct	4202	4261
Query	4060	TGTGGAAATTGAATGGGAGCTGCAGAAAGAAAACAGCAAGCGCTGGAATCCCGAAGTGCA	4119
Sbjct	4262	4321
Query	4120	GTACACATCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATGGACT	4179
Sbjct	4322	4381
Query	4180	TTATACTGAGCCTCGCCCCATTGGCACCCGTTACCTTACCCGTCCCCTGTAATTACGTGT	4239

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Sbjct  4382 ..... 4441
Query  4240 TAATCAATAAACCGGTTGATTTCGTTTCAGTTGAACTTTGGTCTCCTGTCCTTCTTATCTT 4299
Sbjct  4442 ..... 4501
Query  4300 ATCGGTTACCATGGTTATAGCTTACACATTAAGTCTTGGTTGCGCTT 4347
Sbjct  4502 ..... 4549

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>**gb|DQ180604.1|** Adeno-associated virus VR-195 Rep78 (rep78) and capsid protein (cap) genes, complete cds
Length=4259

Score = 6312 bits (3418), Expect = 0.0
Identities = 4002/4282 (93%), Gaps = 48/4282 (1%)
Strand=Plus/Plus

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Query  33      TTTGCGACATTTTTCGACACCATGTGGTCACGCTGGGTATTTAAGCCCGAGTGAGC-ACG 91
Sbjct  1         .....C....C..TT.A.....A..T.G.....G... 59

Query  92      CAGGGTCTCCATTTTGAAGCGGGAGGTTTGAACGCGCAGCCGCCATGCCGGGGTTTTACG 151
Sbjct  60      ....A..C.....~.C..C..AA.....A.....A.....C..C.... 118

Query  152     AGATTGTGATTAAAGTCCCCAGCGACCTTGACGGGCATCTGCCCGGCATTTCTGACAGC- 210
Sbjct  119     ....C.....C.....G..G.....G....A...C.....G.....~T.G 177

Query  211     TTTGTGAACCTGGGTGGCCGAGAAGGAATGGGAGTTGCCGCCAGATTCTGACATGGATCTG 270
Sbjct  178     .....C.....C.....G.....C....C..G..... 237

Query  271     AATCTGATTGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGACTTTCT-GAC 329
Sbjct  238     .....C.....C.....C.....G..T. 297

Query  330     GGAATGGCGCCGIGTGAGTAAGGCCCGGAGGCCCTTTTCTTTGTGCAATTGAGAAGGG 389
Sbjct  298     ~C.....C.....C.....C.....T..G..C..... 356

Query  390     AGAGAGCTACTTCCACATGCACGTGCTCGTGGAACACCACGGGGTGAAATCCATGGTTTT 449
Sbjct  357     C...TC.....C.C..TA.T..G.....G.....G.....C.....GC. 416

Query  450     GGGACGTTTCTGAGTCAGATTTCGCAAAAACCTGATTAGAGAATTTACCGCGGGATCGA 509
Sbjct  417     ...C..C...T.....A.G..C..G...G.G....CC..C..... 476

Query  510     GCCGACTTTGCCAAACTGGTTCGCGGTACAAAGAC-CAGAAATGGCGCCGGAGGCGGGA 568
Sbjct  477     .....CC....C.....G..C.....G...~T.....G.... 535

Query  569     ACAAGGTGGTGGATGAGTGCTACATCCCCAATTACTTGTCTCCCAAAACCCAGCCTGAGC 628
Sbjct  536     .....C.....C....C.C..G.....G..T.....C.... 595

Query  629     TCCAGTGGGCGTGGACTAATATGGAACAGTATTTAAGCGCCTGTTTGAATCTCACGGAGC 688
Sbjct  596     .G.....C.....GG.....A.....G.....C..GG.C.... 655

Query  689     GTAAACGGTTGGTGGCGCAGCATCTGACGCACGTGTC-G-CAGACGCAGGAGCAGAACAA 746
Sbjct  656     .C.....C.C.....C.....C...~...A.C.....C..... 713

Query  747     AGAGAATCAGAATCCCAATTCTGATGCGCCGGTGATCAGATCAAAAACCTCAGC-CAGGT 805
Sbjct  714     G.....T...C.....C.....T..C...C.G.....C..C..G...~C. 772

Query  806     ACATGGAGCTGGTCGGGTGGCTCGTGGACAAGGGG-ATTACCTCGGAGAAGCAGTGGATC 864
Sbjct  773     .....G.....~C....C..C.....C..... 831

Query  865     CAGGAGGACCAGGCCTCATACATCTCCTTCAATGCGGCCTCCAACCTCGCGGTCCCAAATC 924
Sbjct  832     .....G.....C..C.....G... 891

Query  925     AAGGCTGCCT-TGGACAATGCGGGAAAGATTATGAGC-CTGACTAAAACCGCCCCGACT 982
Sbjct  892     .....C...~C.....C..C.....C...~...G.....C...T....G..... 949

Query  983     ACCTGGT-GGGCCAGCAGCC-CGTGGAGGACATTTCCAGCAATCGGATTTATAAAATTTT 1040
Sbjct  950     .....A..C..C...~T..T..~CC.C.....AAA.C...C..C..C..CCGC..CC. 1007

Query  1041     GGAACATAACCGGTACGATCCC--CAATAIG-CGGCTTCCGTCTTTCTGGGATGGG-CCA 1096
Sbjct  1008     ...G..G.....C.....~...TG..~C..C.C.....~.....C..C....C... 1064

Query  1097     CGAAAAAGTTTCGGCAAGAGGAACACCATCTGGCTGTTTGGGCCTGCAACTACCGGG-AAG 1155
Sbjct  1065     ~....CG.....G...C.C.....G...C..C..~....C... 1122

Query  1156     ACCAACATCGCGGAGGCCATAGCCACACITGTGCCCTTCTACGGGTGCGTAAACTGGACC 1215
Sbjct  1123     .....A.....C.....G.C.....C.....C..... 1182

Query  1216     AATGAGAACTTTCCCTTCAACGACTGTGTGACAAAGATGGTGATCTGGTGGGAGGAGGGG 1275
Sbjct  1183     .....T..C.....C..... 1242

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Query	1276	AAGATGACCGCCAAGGTCGTGGAGTCGGCCAAAGCCATTCTGGGAGGAAGCAAGGTGCGC	1335
Sbjct	1243G.....C.....G.....C..C.....	1302
Query	1336	GTGGACCAGAAA-TGCAAGTCCTCGGCCAGATAGA-CCCGACTCCCGTGATCGTCACCT	1393
Sbjct	1303~...G.....G..C.....C..T...~..C.....	1360
Query	1394	CCAACACCAACATGTGCGCCGTGATTGACGGGAAC-TCAACGACCTTCGAACACCAGCAG	1452
Sbjct	1361AG...C.....G.....	1419
Query	1453	CCGTTGCAAGACCGGATGTTCAAATTTGAACTCACCCGCCGTCTGGATCATGACTTTGGG	1512
Sbjct	1420G.....G.....C	1479
Query	1513	AAGGTCACCAAGCAGGAAGTCAAAGACTTTTTCCGGTGGGCAAAGGATCACGTGGTTGAG	1572
Sbjct	1480G..A.....G..C.....C.....GC.....ACC...	1539
Query	1573	GTGGAGCATGAATTCTACGTCAAAAAGGGTGGAGCCAAGAAAAGACCCGCCCCAG-TGA	1631
Sbjct	1540C.....G.....G.....C.....~.A...	1598
Query	1632	CGCAGATATAAGTGAGCCCAAACGGGTGC-GCGAGTCAGTTGCGCAGCCATCGACGTCAG	1690
Sbjct	1599	...G....A...C.....G....~C..T..CCC.....C...G..T.....	1657
Query	1691	ACGCGG-A--AGCTTCGATCAACTACGCAGACAGGTACCAAAACAAATGTTCTCGTCACG	1747
Sbjct	1658A.GG....C..G.GG...TT..C.....	1717
Query	1748	CGGGCATGCTTCAGATGCTGTTTCCCTGCAAGACATGCGAGAGAATGAATCAGAATTTCA	1807
Sbjct	1718	1777
Query	1808	ACATTTGCTTCACGCACGGGACGAGAGACTGTTTCAGAGTGCTTCCCCGGCGTGTGAGAAT	1867
Sbjct	1778C.....A..T.....	1837
Query	1868	CTCAACCGGTGCTCAGAAAGAGGACGTATCGGAACTCTGTGCCATTATCATCTGCTGG	1927
Sbjct	1838A.....G.....	1897
Query	1928	GGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGTGGACCTGGATGACT	1987
Sbjct	1898	1957
Query	1988	GTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATGGTTATCTTCCAGAT	2047
Sbjct	1958C.....	2017
Query	2048	TGGCTCGAGGACAACCTCTCTGAGGGCATTGCGAGTGGTGGGACTTGAAACCTGGAGCC	2107
Sbjct	2018	2077
Query	2108	CCGAAGCCCAAAGCCAACCAGCAAAGCAGGACGACGGCCGGGTCTGGTGCTTCCTGGC	2167
Sbjct	2078A.....	2137
Query	2168	TACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGGCGGAC	2227
Sbjct	2138	2197
Query	2228	GCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAGCGGGTGACAATCCG	2287
Sbjct	2198	2257
Query	2288	TACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCT	2347
Sbjct	2258	2317
Query	2348	TTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTC	2407
Sbjct	2318T..T	2377
Query	2408	GGTCTGGTTGAGGAAGGCGCTAAGACGGCTCCTGGAAAGAAACGTCCGGTAGAGCAGTCG	2467
Sbjct	2378	2437
Query	2468	CCACAAGAGCCAGACTCCTCCTCGGGCATCGGCAAGACAGGCCAGCAGCCCGCTAAAAAG	2527
Sbjct	2438	2497
Query	2528	AGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGATCCACAACCTCTCGGA	2587
Sbjct	2498C.....	2557
Query	2588	GAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGTGGCGCA	2647
Sbjct	2558	2617
Query	2648	CCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCTCAGGAAATTGGCAT	2707
Sbjct	2618	2677
Query	2708	TGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCCGCACCTGGGCCTTG	2767
Sbjct	2678	2737
Query	2768	CCCACCTACAATAACCACCTCTACAAGCAAATCTCCAGTGCTTCAACGGGGGCCAGCAAC	2827
Sbjct	2738	2797
Query	2828	GACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATTTCACAGATTCCAC	2887
Sbjct	2798	2857

Query	2888	TGCCACTTTTCACCACGTGACTGGCAGCGACTCATCAACAACAATTGGGGATTCCGGCCCC	2947
Sbjct	2858G.....	2917
Query	2948	AAGAGACTCAACTTCAAACCTCTTCAACATCCAAGTCAAGGAGGTCACGACGAATGATGGC	3007
Sbjct	2918G.....G.....	2977
Query	3008	GTCACAACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTCTCGGACTCGGAGTAC	3067
Sbjct	2978	3037
Query	3068	CAGCTTCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTCCGTTCCCGGCGGAC	3127
Sbjct	3038	3097
Query	3128	GTGTTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGCAGCCAAGCCGTGGGA	3187
Sbjct	3098	3157
Query	3188	CGTTTCATCCTTTTACTGCCTGGAATATTTCCCTTCTCAGATGCTGAGAACGGGCAACAAC	3247
Sbjct	3158	3217
Query	3248	TTTACCTTCAGCTACACCTTTGAGGAAGTGCCTTTCCACAGCAGCTACGCGCACAGCCAG	3307
Sbjct	3218	3277
Query	3308	AGCCTGGACCGGCTGATGAATCCTCTCATCGACCAATACCTGTATTACCTGAACAGAACT	3367
Sbjct	3278	3337
Query	3368	CAAAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCCGTGGGTCTCCAGCT	3427
Sbjct	3338	3397
Query	3428	GGCATGCTCTGTTTCAGCCAAAACTGGCTACCTGGACCTGTTATCGGCAGCAGCGCGTT	3487
Sbjct	3398	3457
Query	3488	TCTAAAACAAAAACAGACAACAACAACAGCAATTTTACCTGGACTGGTGCTTCAAAATAT	3547
Sbjct	3458G.....	3517
Query	3548	AACCTCAATGGGCGTGAATCCATCATCAACCCTGGCACTGCTATGGCCTCACACAAAGAC	3607
Sbjct	3518A.....	3577
Query	3608	GACGAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTTGAAAAGAGAGCGCCGGA	3667
Sbjct	3578	3637
Query	3668	GCTTCAAACACTGCATTGGACAATGTCATGATTACAGACGAAGAGGAAATTAAAGCCACT	3727
Sbjct	3638	3697
Query	3728	AACCCTGTGGCCACCGAAAGATTTGGGACCGTGGCAGTCAATTTCCAGAGCAGCAGCACA	3787
Sbjct	3698	3757
Query	3788	GACCCTGCGACCGGAGATGTGCAATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGAT	3847
Sbjct	3758	C.....T.....	3817
Query	3848	AGAGACGTGTACCTGCAGGGTCCCATTGGGCCAAAATTCCTCACACAGATGGACACTTT	3907
Sbjct	3818C.....	3877
Query	3908	CACCCGTCTCCTCTTATGGGCGGCTTTGGACTCAAGAACCCGCCTCCTCAGATCCTCATC	3967
Sbjct	3878C.....	3937
Query	3968	AAAAACACGCCTGTTCTGCGAATCCTCCGGCGGAGTTTTTCAGCTACAAAGTTTGCTTCA	4027
Sbjct	3938	3997
Query	4028	TTCATCACCCAATACTCCACAGGACAAGTGAGTGTGGAAATTGAATGGGAGCTGCAGAAA	4087
Sbjct	3998	4057
Query	4088	GAAAACAGCAAGCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAATCTGCC	4147
Sbjct	4058	4117
Query	4148	AACGTTGATTTTACTGTGGACAACAATGGACTTTATACTGAGCCTCGCCCCATTGGCACC	4207
Sbjct	4118C.....	4177
Query	4208	CGTTACCTTACCCGTCCCCTGTAATTACGTGTTAATCAATAAACCGGTTGATTGTTTTCA	4267
Sbjct	4178	4237
Query	4268	GTTGAACTTTGGTCTCCTGTCC	4289
Sbjct	4238	4259

>gb|AF028704.1|AF028704 Adeno-associated virus 6, complete genome
Length=4683

Score = 6270 bits (3395), Expect = 0.0
Identities = 4054/4370 (92%), Gaps = 53/4370 (1%)
Strand=Plus/Plus